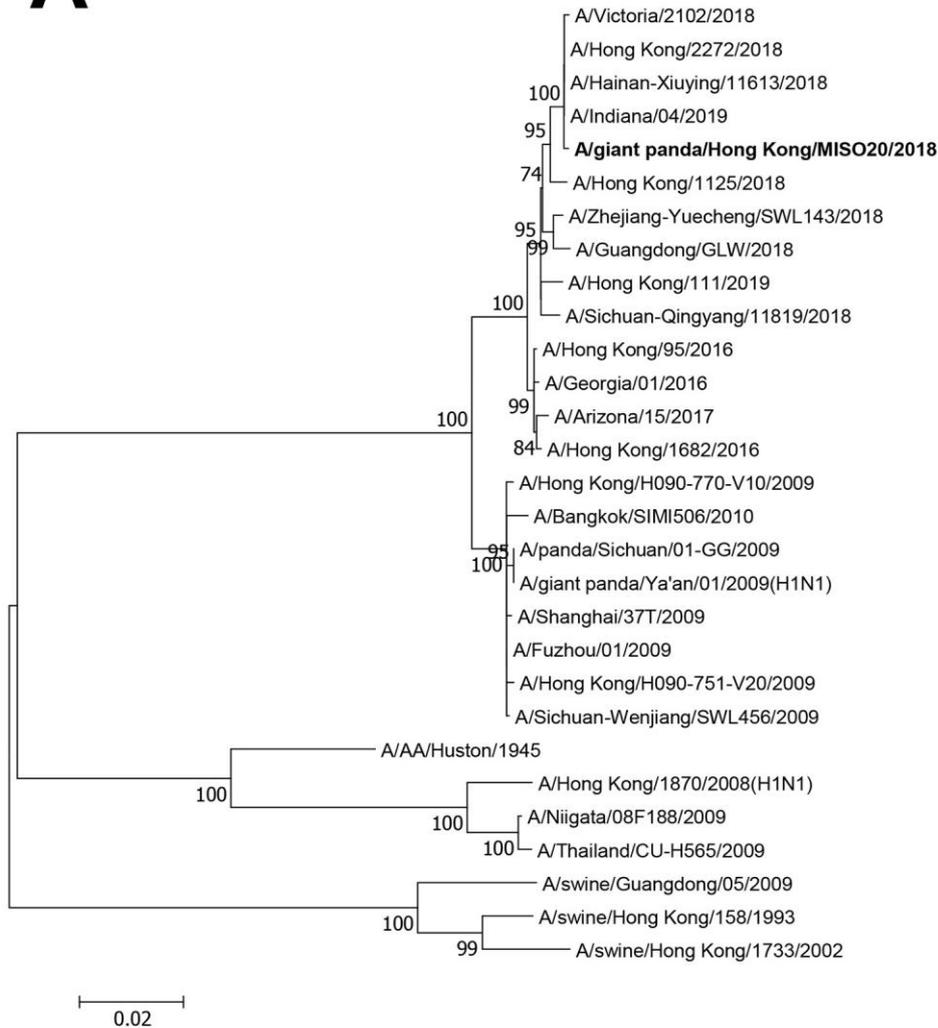


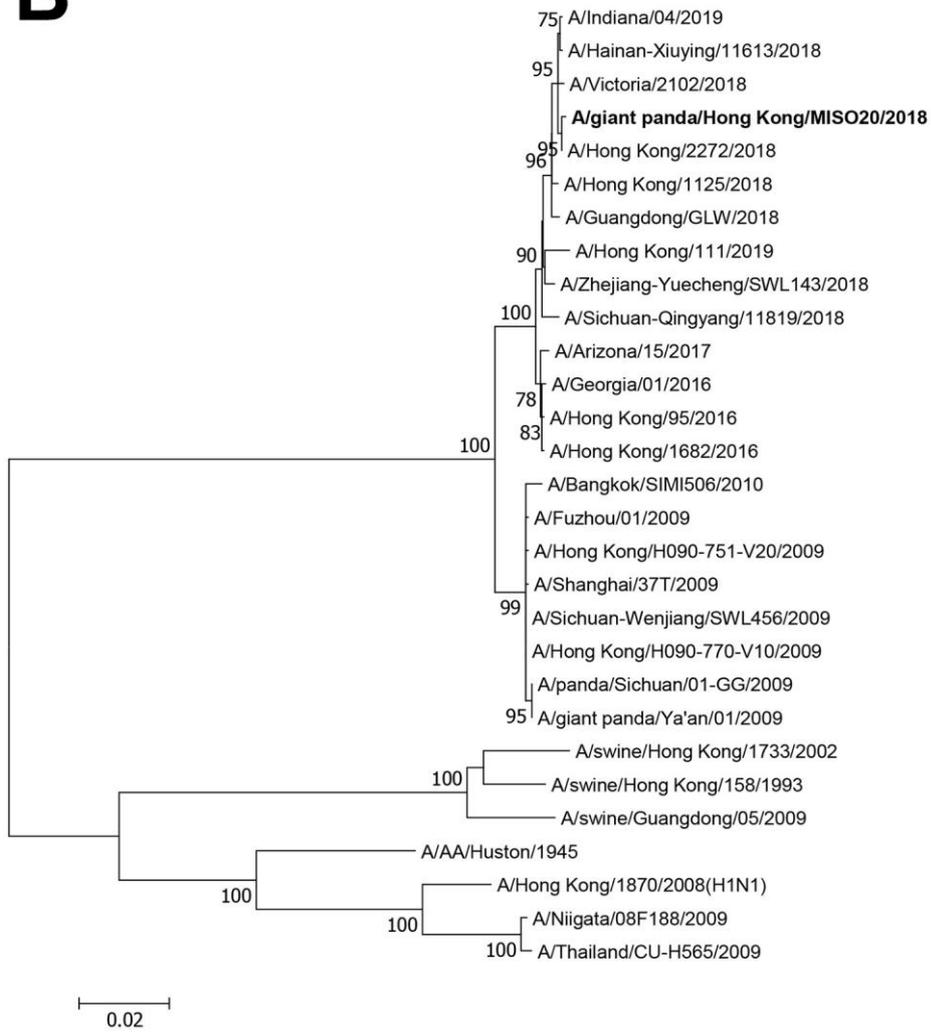
Influenza A(H1N1)pdm09 Virus Infection in a Captive Giant Panda, Hong Kong

Appendix

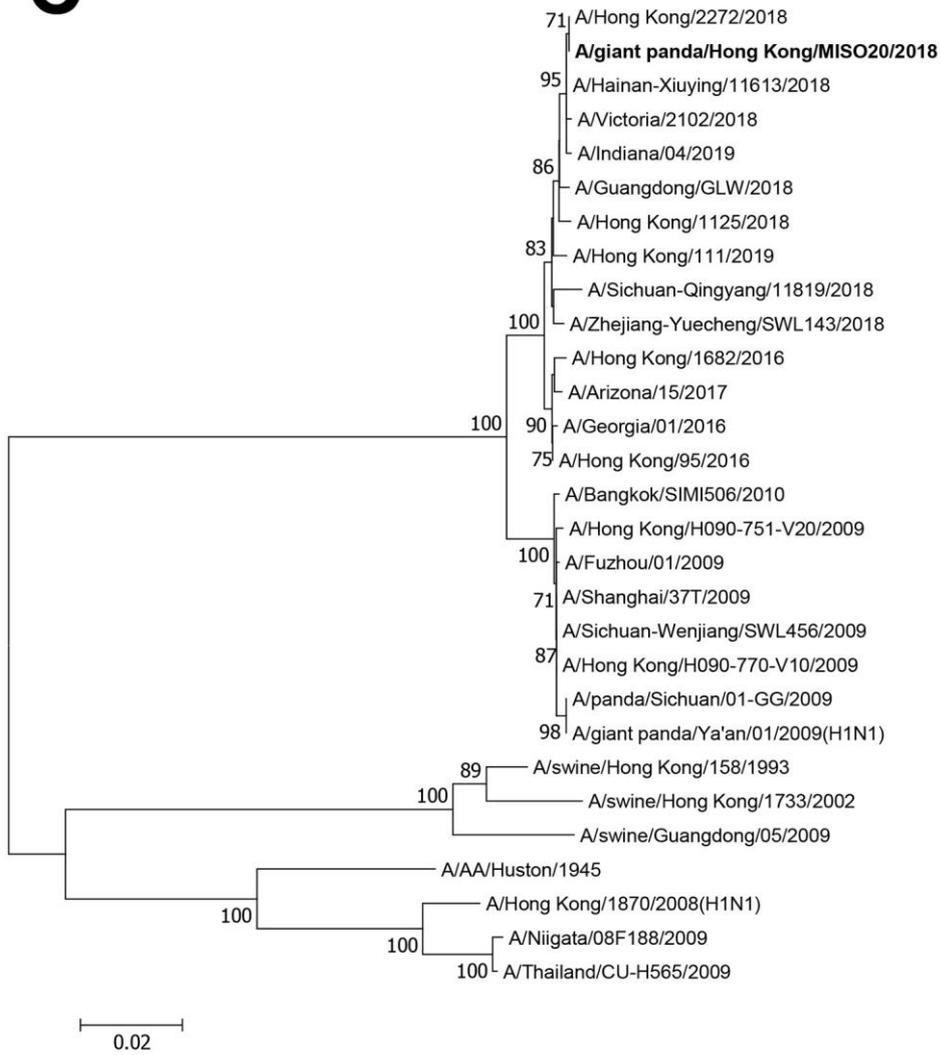
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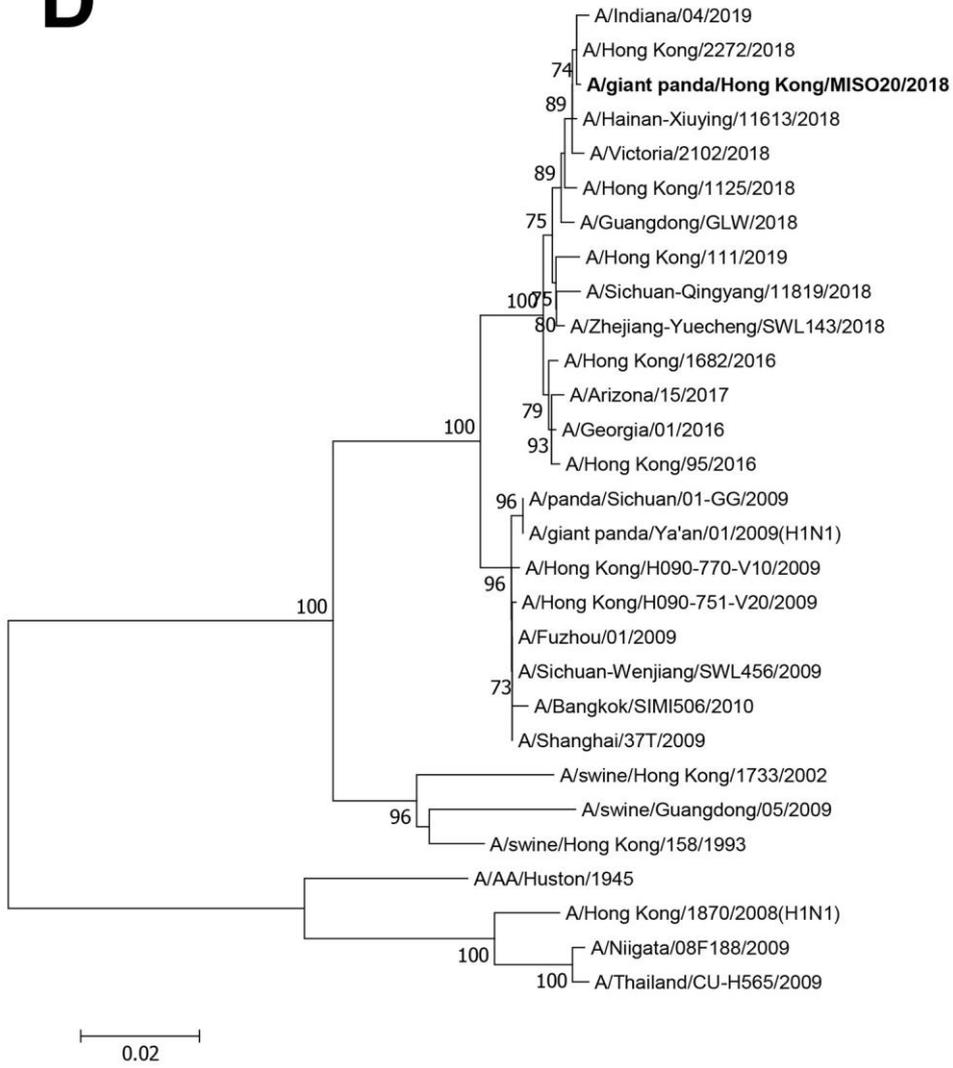
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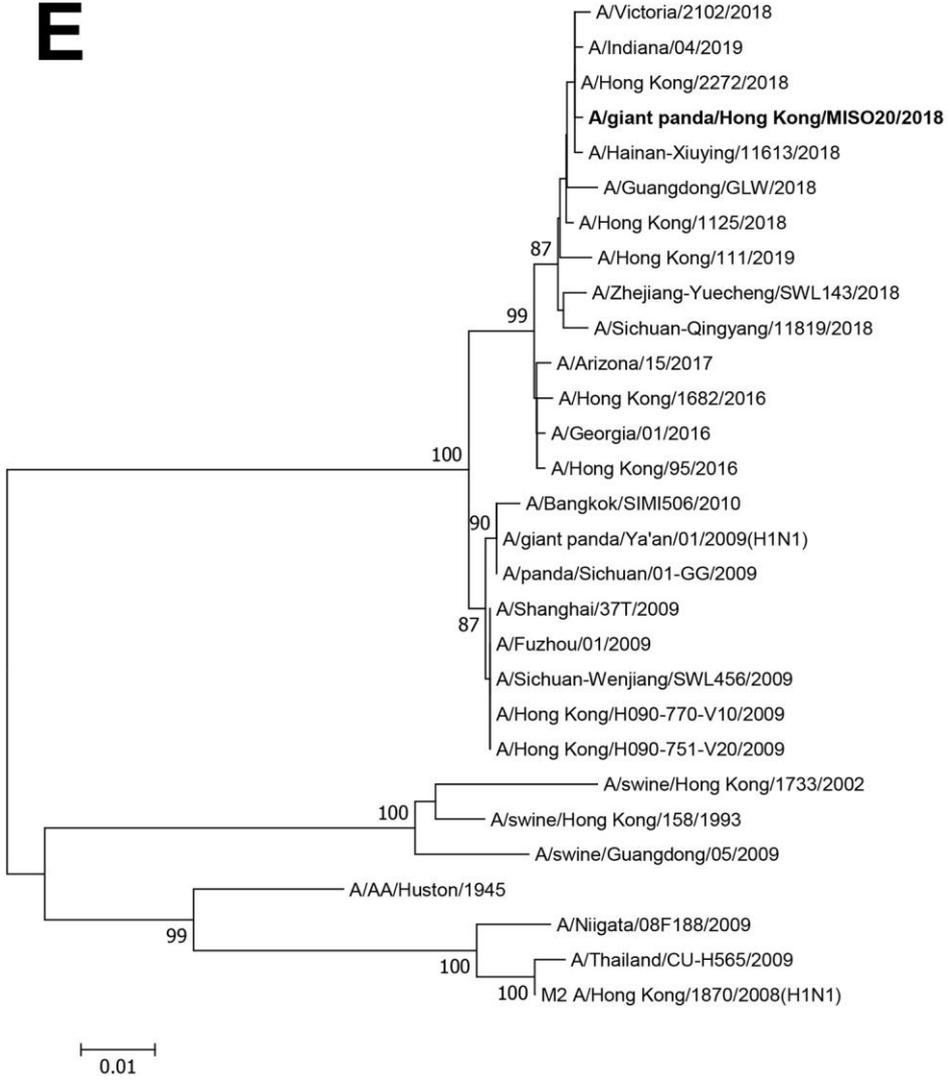
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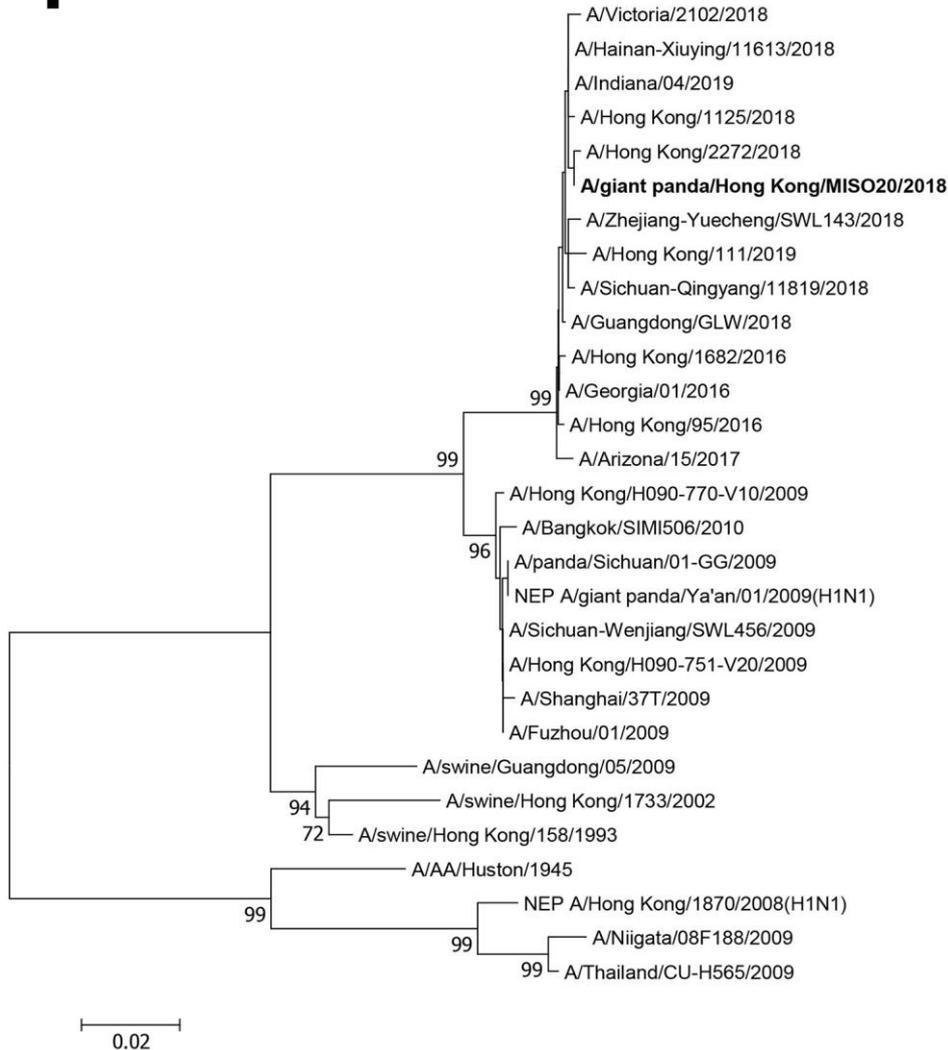
D



E



F



Appendix Figure. Phylogenetic analyses of 6 gene sequences of influenza A(H1N1)pdm09 (**A/giant panda/Hong Kong/MISO20/2018**) isolated from a giant panda and other previously characterized pH1N1. The trees were constructed by the neighbor-joining method using Kimura 2-parameter in MEGA6. The analyses included 2,238 nt positions in polymerase basic protein 2 (A), 2,262 in polymerase basic protein 1(B), 2,145 in polymerase acidic protein (C), 1,492 in nucleoprotein (D), 971 in matrix protein (E), and 824 in nonstructural protein gene sequences. Scale bars indicate nucleotide substitutions per site. Bootstrapping was performed with 1,000 replicates; only bootstrap values ≥ 700 are shown. Bold text indicates the giant panda isolate in this study.